

Supporting Information

Arthpyrones A–C, Pyridone Alkaloids from a Sponge-Derived Fungus *Arthrinium arundinis* ZSDS1-F3

Junfeng Wang,[†] Xiaoyi Wei,[‡] Xiaochu Qin,[§] Xiuping Lin,[†] Xuefeng Zhou,[†] Shengrong Liao,[†] Bin Yang,[†] Juan Liu,[†] Zhengchao Tu,[§] and Yonghong Liu^{*,†}

[†] CAS Key Laboratory of Tropical Marine Bio-resources and Ecology/Guangdong Key Laboratory of Marine Materia Medica/RNAM Center for Marine Microbiology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou 510301, China

[‡] Key Laboratory of Plant Resources Conservation and Sustainable Utilization, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650, China

[§] Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou 510530, China

List of Supporting Information

List of contents	Page
Experimental details.....	S2
Computational details.....	S7
Figure S8. The ¹ H NMR spectrum of arthpyrone A (1) in CD ₃ OD.....	S12
Figure S9. The ¹³ C NMR spectrum of arthpyrone A (1) in CD ₃ OD.....	S13
Figure S10. The HMQC spectrum of arthpyrone A (1) in CD ₃ OD.....	S14
Figure S11. The ¹ H- ¹ H COSY spectrum of arthpyrone A (1) in CD ₃ OD.....	S15
Figure S12. The HMBC spectrum of arthpyrone A (1) in CD ₃ OD.....	S16
Figure S13. The NOESY spectrum of arthpyrone A (1) in CD ₃ OD.....	S17
Figure S14. The HRESIMS spectrum of arthpyrone A (1).....	S18
Figure S15. The ¹ H NMR spectrum of arthpyrone B (2) in CD ₃ OD.....	S19
Figure S16. The ¹³ C NMR spectrum of arthpyrone B (2) in CD ₃ OD.....	S20
Figure S17. The HMQC spectrum of arthpyrone B (2) in CD ₃ OD.....	S21
Figure S18. The ¹ H- ¹ H COSY spectrum of arthpyrone B (2) in CD ₃ OD.....	S22

Figure S19. The HMBC spectrum of arthpyrone B (2) in CD ₃ OD.....	S23
Figure S20. The NOESY spectrum of arthpyrone B (2) in CD ₃ OD.....	S24
Figure S21. The HRESIMS spectrum of arthpyrone B (2).....	S25
Figure S22. The ¹ H NMR spectrum of arthpyrone C (3) in CD ₃ OD.....	S26
Figure S23. The ¹³ C NMR spectrum of arthpyrone C (3) in CD ₃ OD.....	S27
Figure S24. The HMQC spectrum of arthpyrone C (3) in CD ₃ OD.....	S28
Figure S25. The ¹ H- ¹ H COSY spectrum of arthpyrone C (3) in CD ₃ OD.....	S29
Figure S26. The HMBC spectrum of arthpyrone C (3) in CD ₃ OD.....	S30
Figure S27. The NOESY spectrum of arthpyrone C (3) in CD ₃ OD.....	S31
Figure S28. The HRESIMS spectrum of arthpyrone C (3).....	S32
Figure S29. Analyzed compounds 1 and 2 by a chiralcel OD-H column	S33

Experimental details

General Experimental Procedures. Optical rotations were measured with a PerkinElmer 341 polarimeter. UV spectra were recorded on a Shimadzu UV-2401PC spectrometer. IR spectra were measured on JASCO FT/IR-480 plus spectrometer with KBr pellets. ¹H, ¹³C NMR, DEPT, and 2D-NMR spectra were recorded on the Bruker DRX-500 spectrometer using TMS as internal standard and chemical shifts were recorded as δ -values. HRESIMS (including ESIMS) spectra were recorded on an Applied Biosystems Mariner 5140 spectrometer. X-ray diffraction intensity data were collected on a CrysAlis PRO CCD area detector diffractometer with graphite monochromated Cu K α radiation (λ = 1.54178Å). TLC and column chromatography (CC) were performed on plates precoated with silica gel GF₂₅₄ (10–40 μ m) and over silica gel (200–300 mesh) (Qingdao Marine Chemical Factory, China), and Sephadex LH-20 (Amersham Biosciences, Sweden), respectively. All solvents used were of analytical grade (Tianjin Fuyu Chemical and Industry Factory). Semipreparative HPLC was performed using an ODS column (YMC-pack ODS-A, 10 \times 250 mm, 5 μ m, 4 mL/min).

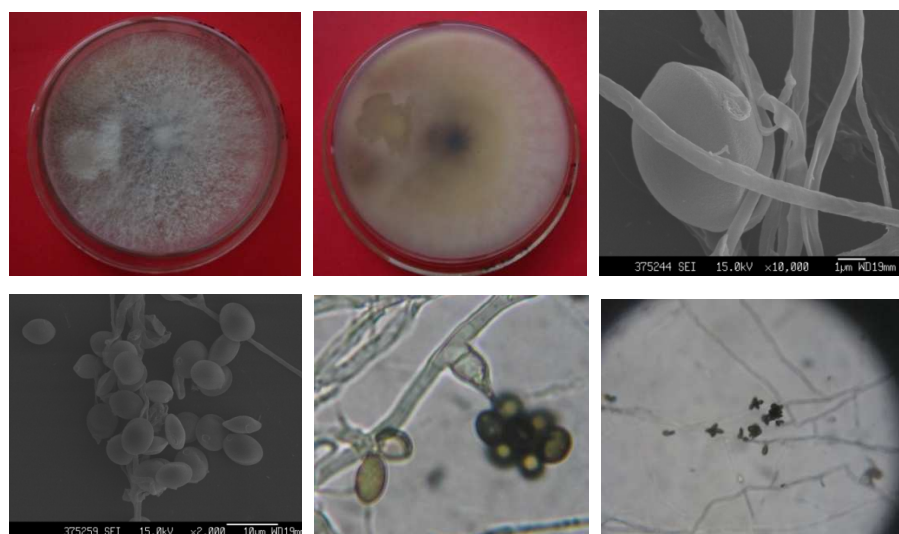


Figure S1. Colony appearance and micromorphology of strain *A. arundinis* ZSDS1-F3

The ITS gene sequence data of *Arthrinium arundinis* ZSDS1-F3

TCCGTAGGTGAACCTGCGGAGGGATCATTACAGAGTTATACAACCTCCCATAC
 CATTTGTTAACCTACCCAGTTATGCCTCGGCGTAAGCTCGGTTGGAGGCACCTG
 CAGCTACCCTGTAGTTGCACCCGCAGCTACCCTGTAGTTGTTGGTGCAGCTACC
 CTGTAGTTGCGGACTGCCAACTCCAGCCGCGGCCCGCCGGCGGTACACTAAAC
 TCTGTTTTATTTTATATTCTGAGCGTCTTATTTTAATAAGTTAAAACTTTCAACA
 ACGGATCTCTTGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTA
 ATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCC
 ATCAGTATTCTGGTGGGCATGCCTGTTTCGAGCGTCATTTCAACCCTTAAGCCTA
 GCTTAGTGTTGGGAATCTGCTGTACTGCAGTTCCTTAAAGACAGTGGCGGAGC
 GGCGGTAGTCCTCTGAGCGTAGTAATTTATTTCTCGCTTTTGTCAGGCTCTGTCC
 TCCCGCCATAAAACCCCAATTTTTTAGTGGTTGACCTCGGATCAGGTAGGAAT
 ACCCGCTGAACTTAAGCATATCAATAA

Fungal Material. The fungal strain, *A. arundinis* ZSDS1-F3, was isolated from the sponge *Phakellia fusca* Thiele, which was collected from the Xisha Islands of China in 2012, and identified by Professor Houwen Lin, Second Military Medical University. A voucher specimen (No. 12071301) was deposited in the CAS Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of

Sciences, Guangzhou, China. The frozen sample was defrosted in sterile distilled water and washed with sterile distilled water. The washed sample (1 g) was ground with sterile distilled water (10 mL) and then was diluted to 10^{-3} g/mL, 100 μ L of which was dispersed across a solid phase agar plate (Czapek's media) and incubated at 28 °C for 7 days. On the marginal zone, gray-white colonies were observed. A single colony was transferred onto Czapek's media. It was identified according to its morphological characteristics (Figure S1) and ITS gene sequences (GenBank Accession No. KF693784). This strain has been deposited in China General Microbiological Culture Collection Center with a deposition number CGMCC 8652. A reference culture is deposited in at our laboratory at -80 °C. The producing strain was prepared on potato dextrose agar slants at 3.3% salt concentration and stored at 4 °C.

Fermentation and Extraction. *A. arundinis* ZSDS1-F3 was incubated on a rotary shaker (180 rpm) at 28°C for 12 days in 1000 mL \times 150 conical flasks containing the liquid medium (300 mL/flask) composed of sorbitol (20 g/L), maltose (20 g/L), MSG (10 g/L), KH_2PO_4 (0.5 g/L), $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ (0.3 g/L), yeast extract (3 g/L). The fermented whole broth (45 L) was filtered through cheesecloth to separate it into filtrate and mycelia. The filtrate was concentrated under vacuum to about a quarter of original volume and then extracted three times with EtOAc to give an EtOAc solution, while the mycelia were extracted three times with acetone. The acetone solution was evaporated under reduced pressure to afford an aqueous solution. The aqueous solution was extracted three times with EtOAc to give another EtOAc solution. Both EtOAc solutions were combined and concentrated under vacuum to give an EtOAc extract (95.1 g).

Purification. The EtOAc extract (95.1 g) was subjected to VLC on a silica gel column using step gradient elution with $\text{MeOH}-\text{CH}_2\text{Cl}_2$ (0–100%) to separate into nine fractions based on TLC properties. Fraction 5 was divided into five parts (Frs.5-1–5-5) by Sephadex LH-20 (MeOH). Compounds **3** (8.0 mg, t_R 20.5 min) was obtained from Fr.5-3 by semipreparative HPLC eluting with 55% Acetonitrile. Fraction 6 was divided into six parts (Frs.6-1–6-6) by Sephadex LH-20 (MeOH). Fr. 6-1 was directly separated by HPLC (72% $\text{MeOH}/\text{H}_2\text{O}$) to yield **1** (28.9 mg, t_R 19.8 min). Fraction 7 was divided into six parts (Frs.7-1–7-6) by Sephadex LH-20 (MeOH). Fr. 7-2 was further divided into six parts

(Frs.7-2-1–7-2-6) by HPLC (50% Acetonitrile/H₂O). Fr. 7-2-1 was purified by HPLC (40% Acetonitrile/H₂O) to yield **2** (6.4 mg, *t_R* 7.6 min). Fr. 7-2-4 was purified by HPLC (75% MeOH/H₂O) to yield **4** (533.2 mg, *t_R* 17.6 min).

Arthpyrone A (1): yellow amorphous solid; $[\alpha]_D^{25} -4.2$ (*c* 2.9, MeOH); UV (MeOH) λ_{\max} (log ϵ): 207 (3.65), 274 (2.82), 320 (2.95) nm; IR (KBr) ν_{\max} 3321, 1682, 1639, 1535, 1431, 1373, 1204, 1138, 1111, 1026 cm⁻¹; ¹H NMR and ¹³C NMR data, see Table 1; HRESIMS *m/z* 446.2169 [M + H]⁺ (calcd for C₂₄H₃₂NO₇, 446.2173).

Arthpyrone B (2): yellow amorphous solid; $[\alpha]_D^{25} -7.0$ (*c* 0.6, MeOH); UV (MeOH) λ_{\max} (log ϵ): 202 (3.39), 219 (3.39), 311 (2.78) nm; IR (KBr) ν_{\max} 3460, 1690, 1643, 1531, 1435, 1315, 1207, 1134, 1096, 1038 cm⁻¹; ¹H NMR and ¹³C NMR data, see Table 1; HRESIMS *m/z* 428.2069 [M - H]⁻ (calcd for C₂₄H₃₀NO₆, 428.2079).

Arthpyrone C (3): yellow amorphous solid; $[\alpha]_D^{25} -68.0$ (*c* 0.7, MeOH); UV (MeOH) λ_{\max} (log ϵ): 204 (3.56), 287 (3.12), 339 (2.94) nm; IR (KBr) ν_{\max} 1639, 1605, 1531, 1435, 1373, 1265, 1215, 1099, 1057 cm⁻¹; ¹H NMR and ¹³C NMR data, see Table 1; HRESIMS *m/z* 460.2320 [M + H]⁺ (calcd for C₂₅H₃₄NO₇, 460.2330).

Table S1. Cytotoxicities against Tumor Cells for **1–4**.

Cell lines	IC ₅₀ (μM)				
	1	2	3	4	TSA
K562	>50	>50	3.5	0.45	0.16
MOLT-4	22	>50	0.87	0.66	0.034
U937	31	>50	1.3	0.24	0.059
MCF-7	>50	>50	5.6	0.99	0.079
Hela	>50	>50	2.1	1.3	0.10
Huh-7	>50	>50	11	2.2	0.089
A549	>50	>50	8.1	1.7	0.053
BGC823	>50	>50	7.6	1.3	0.081
H1975	45	>50	8.6	1.6	0.099
HL60	>50	>50	1.3	0.89	0.082

Table S2. Anti-AchE activities of **1–4**.

Activity	IC ₅₀ (μM)				
	1	2	3	4	Tacrine
Anti-AchE	47	>100	0.81	39	0.48

Cytotoxicity Assay. Cytotoxicity was assayed with the CCK-8 (Dojindo, Japan) method. Cell lines, K562, A549, Huh-7, H1975, MCF-7, U937, BGC823, HL60, Hela, and MOLT-4 were purchased from Shanghai Cell Bank, Chinese Academy of Sciences. Cells were routinely grown and maintained in mediums RPMI or DMEM with 10% FBS and with 1% penicillin/streptomycin. All cell lines were incubated in a Thermo/Forma Scientific CO₂ Water Jacketed Incubator with 5% CO₂ in air at 37 °C. Cell viability assay was determined by the CCK-8 (Dojindo, Japan) assay. Cells were seeded at a density of 400-800 cells/well in 384 well plates and treated with various concentration of compounds or solvent control. After 72 h incubation, CCK-8 reagent was added, and absorbance was measured at 450 nm using Envision 2104 multi-label Reader (Perkin Elmer, USA). Dose response curves were plotted to determine the IC₅₀ values using Prism 5.0 (GraphPad Software Inc., USA). TSA was used as the positive control.

AchE inhibitory Assay. The AchE inhibitory activity was measured according to Ellman's coupled enzyme assay, modified as follow. 0.2Units of AchE were dissolved in 0.1M potassium phosphate buffer (pH 7.4), and purified compounds dissolved in DMSO (the series of final concentrations as 8, 4, 2, 1, 0.5, 0.25 μ M) were added to each well of a 96-well plate. Then, acetylthiocholine iodide and 5,5'-dithiobis(2-nitrobenzoic acid) dissolved in 0.1M potassium phosphate buffer (pH 7.4) were added to reach a final concentration of 50 μ M both. The reaction was carried out at 30 $^{\circ}$ C for 30 min. The absorbance was measured at 410 nm using a spectrophotometer and the half maximum inhibitory concentration (IC₅₀) was calculated. Tacrine was used as the positive control with an IC₅₀ value of 0.48 μ M.

Computational Details

1. Methods

Molecular Merck force field (MMFF) and DFT/TDDFT calculations were performed with Spartan' 14 software package (Wavefunction Inc., Irvine, CA, USA) and Gaussian09 program package,¹ respectively, using default grids and convergence criteria. MMFF conformational search generated low-energy conformers within a 10 kcal/mol energy window were subjected to geometry optimization using DFT method at the B3LYP/6-31G (d) level. Frequency calculations were run at the same level to verify that each optimized conformer was a true minimum and to estimate their relative thermal free energies (ΔG) at 298.15K. Energies of the low-energy conformers in MeOH were calculated at the B3LYP/6-311+G (d,p) level. Solvent effects were taken into account by using polarizable continuum model (PCM). The TDDFT calculations were performed using the long-range corrected hybrid CAM-B3LYP and the hybrid B3LYP functionals, and Ahlrichs' basis sets SVP (split valence plus polarization)² and TZVP (triple zeta valence plus polarization).³ The number of excited states per each molecule was 36. The CD spectra were generated by the program SpecDis⁴ using a Gaussian band shape with 0.23–0.45 eV exponential half-width from dipole-length dipolar and rotational strengths; the difference with dipole-velocity values was negligible (<10%) for most transitions. Equilibrium population of each conformer at 298.15K was calculated from its relative free energies using Boltzmann statistics. The calculated spectra of compounds **1–4** were generated from the low-energy conformers according to the Boltzmann weighting of each conformer in MeOH solution.

2. Results

Table S3. Relative and free energies^a and equilibrium populations^b of low-energy conformers of **1–4** in MeOH.

conformer	ΔE	ΔG	P (%)
Compound 1			
1a	0.00	0.00	76.7
1b	1.23	0.92	15.8
1c	1.59	1.73	3.9
1d	1.66	1.79	3.5
Compound 2			
2a	0.00	0.00	73.9
2b	1.21	0.95	14.9
2c	1.42	1.46	6.3
2d	1.51	1.61	4.9
Compound 3			
4a	0.00	0.00	64.4
4b	0.63	0.44	30.6
4c	1.28	1.55	4.7
4d ^c	3.15	3.13	0.3
Compound 4			
5a	0.00	0.00	39.9
5b	0.45	0.20	28.5
5c	0.36	0.40	20.2
5d	1.10	0.74	11.4

^aAt the B3LYP/6-311+G(d,p) level, in kcal/mol. ^bFrom ΔG values at 298.15 K. ^cConformer not used for ECD/TDDFT calculations.

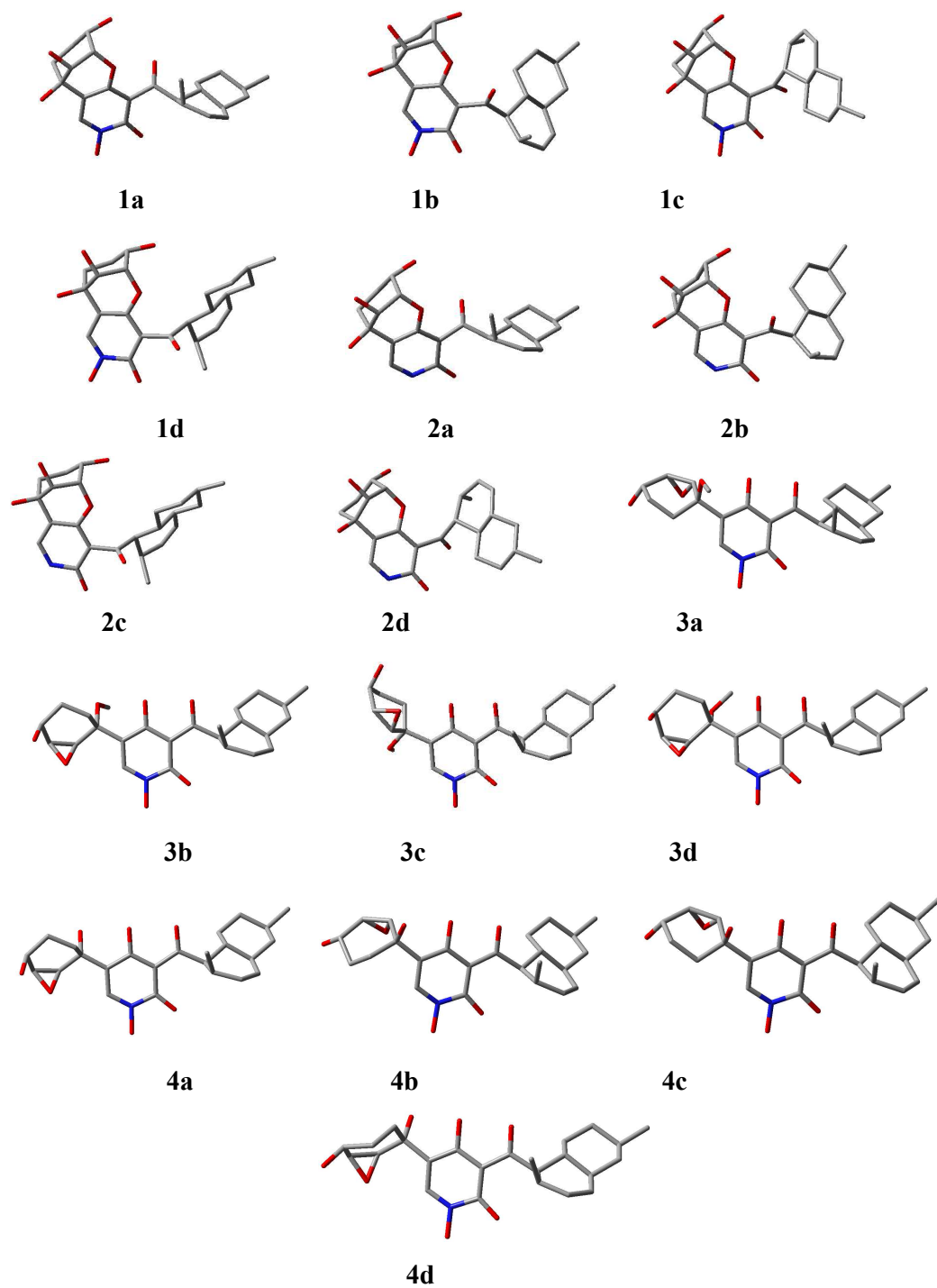


Figure S2. Conformations of low-energy conformers of 1–4.

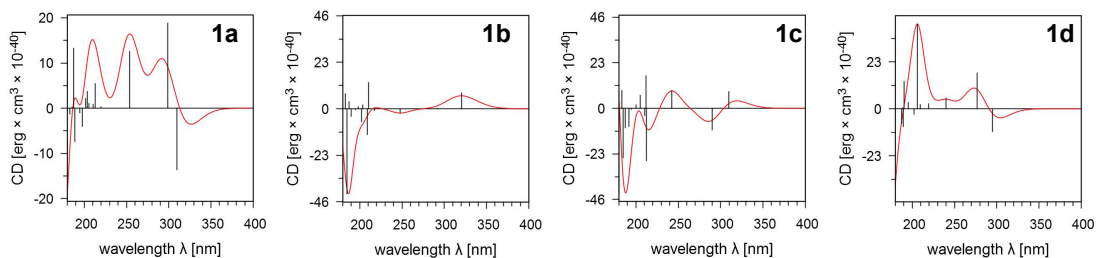


Figure S3. Calculated ECD spectra of the low-energy conformers of **1** in MeOH using the CAM-B3LYP/SVP method. Vertical bars represent rotational strengths R . $\sigma = 0.30$ eV; shift = ± 0 nm.

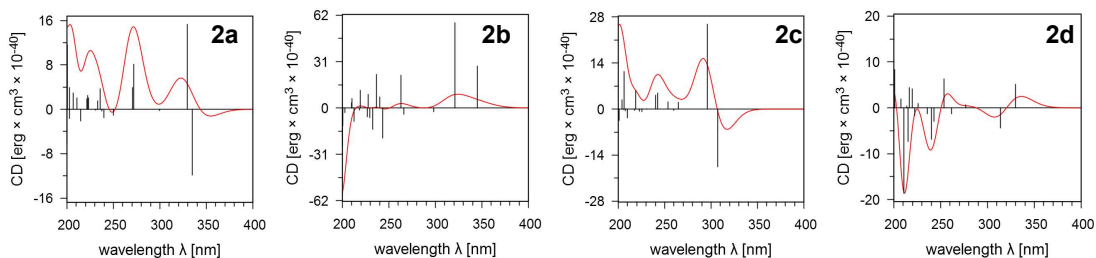


Figure S4. Calculated ECD spectra of the low-energy conformers of **2** in MeOH using the B3LYP/TZVP method. Vertical bars represent rotational strengths R . $\sigma = 0.23$ eV; shift = ± 0 nm.

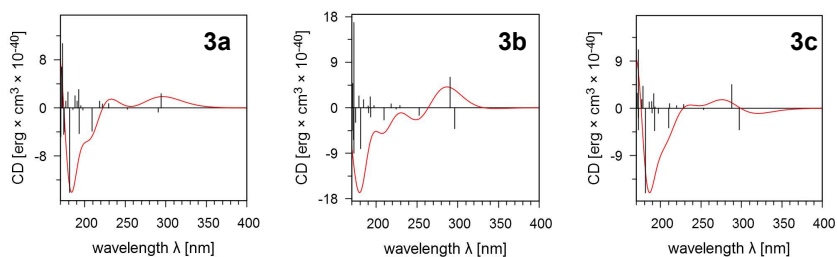


Figure S5. Calculated ECD spectra of the low-energy conformers of **3** in MeOH using the CAM-B3LYP/SVP method. Vertical bars represent rotational strengths R . $\sigma = 0.45$ eV; shift = ± 0 nm.

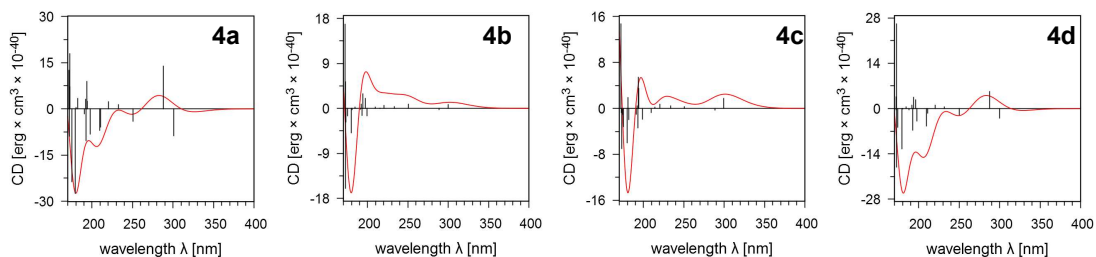


Figure S6. Calculated ECD spectra of the low-energy conformers of **4** in MeOH using the CAM-B3LYP/SVP method. Vertical bars represent rotational strengths R . $\sigma = 0.40$ eV; shift = ± 0 nm.

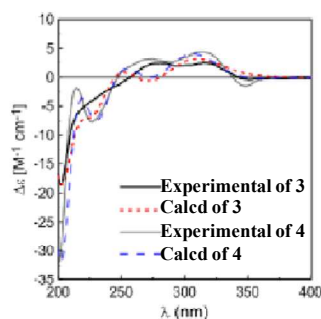


Figure S7. Comparison between calculated (CAM-B3LYP/SVP) and experimental ECD spectra of **3** and **4** in MeOH.

3. References

- (1) Frisch, M. J.; Trucks, G. W.; Schlegel, H. B.; Scuseria, G. E.; Robb, M. A.; Cheeseman, J. R.; Scalmani, G.; Barone, V.; Mennucci, B.; Petersson, G. A.; Nakatsuji, H.; Caricato, M.; Li, X.; Hratchian, H. P.; Izmaylov, A. F.; Bloino, J.; Zheng, G.; Sonnenberg, J. L.; Hada, M.; Ehara, M.; Toyota, K.; Fukuda, R.; Hasegawa, J.; Ishida, M.; Nakajima, T.; Honda, Y.; Kitao, O.; Nakai, H.; Vreven, T.; Montgomery, J. A.; Peralta, J. E.; Ogliaro, F.; Bearpark, M.; Heyd, J. J.; Brothers, E.; Kudin, K. N.; Staroverov, V. N.; Keith, T.; Kobayashi, R.; Normand, J.; Raghavachari, K.; Rendell, A.; Burant, J. C.; Iyengar, S. S.; Tomasi, J.; Cossi, M.; Rega, N.; Millam, J. M.; Klene, M.; Knox, J. E.; Cross, J. B.; Bakken, V.; Adamo, C.; Jaramillo, J.; Gomperts, R.; Stratmann, R. E.; Yazyev, O.; Austin, A. J.; Cammi, R.; Pomelli, C.; Ochterski, J. W.; Martin, R. L.; Morokuma, K.; Zakrzewski, V. G.; Voth, G. A.; Salvador, P.; Dannenberg, J. J.; Dapprich, S.; Daniels, A. D.; Farkas, O.; Foresman, J. B.; Ortiz, J. V.; Cioslowski, J.; Fox, D. J. Gaussian 09, revision C.01. Gaussian, Inc.: Wallingford CT, **2010**.
- (2) Schäfer, A.; Horn, H.; Ahlrichs, R. *J. Chem. Phys.* **1992**, *97*, 2571–2577.
- (3) Schäfer, A.; Huber, C.; Ahlrichs, R. *J. Chem. Phys.* **1994**, *100*, 5829–5835.
- (4) Bruhn, T.; Schaumlöffel, A.; Hemberger, Y.; Bringmann, G. SpecDis Version 1.60. Germany: University of Wuerzburg; **2012**.

[illegible]

Chemical structure of compound 1 is shown above the spectrum. The structure is a complex polycyclic molecule with multiple hydroxyl and carbonyl groups.

Chemical shifts (ppm) are listed on the left side of the spectrum:

- 18.1124
- 23.0255
- 27.7589
- 30.1698
- 33.5372
- 34.2979
- 36.7374
- 37.3861
- 38.0695
- 43.0746
- 43.3963
- 49.8478
- 56.7393
- 69.5849
- 70.5267
- 71.5296
- 85.3853
- 112.7485
- 113.0209
- 131.6913
- 132.7021
- 135.1589
- 159.1348
- 161.9791
- 207.1717

Figure S10. The HMQC spectrum of arthpyrone A (**1**) in CD₃OD

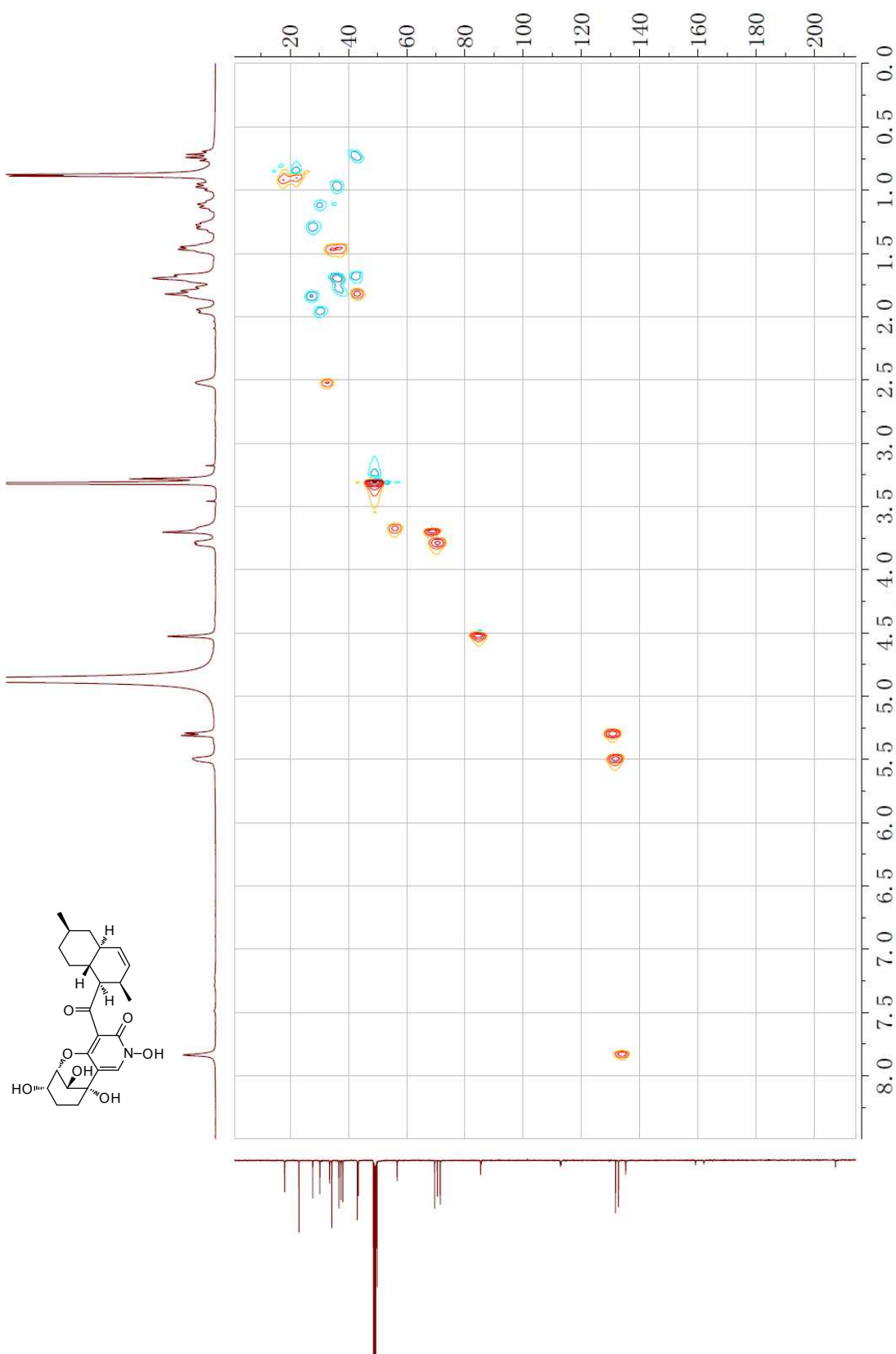


Figure S11. The ^1H - ^1H COSY spectrum of arthpyrone A (**1**) in CD_3OD

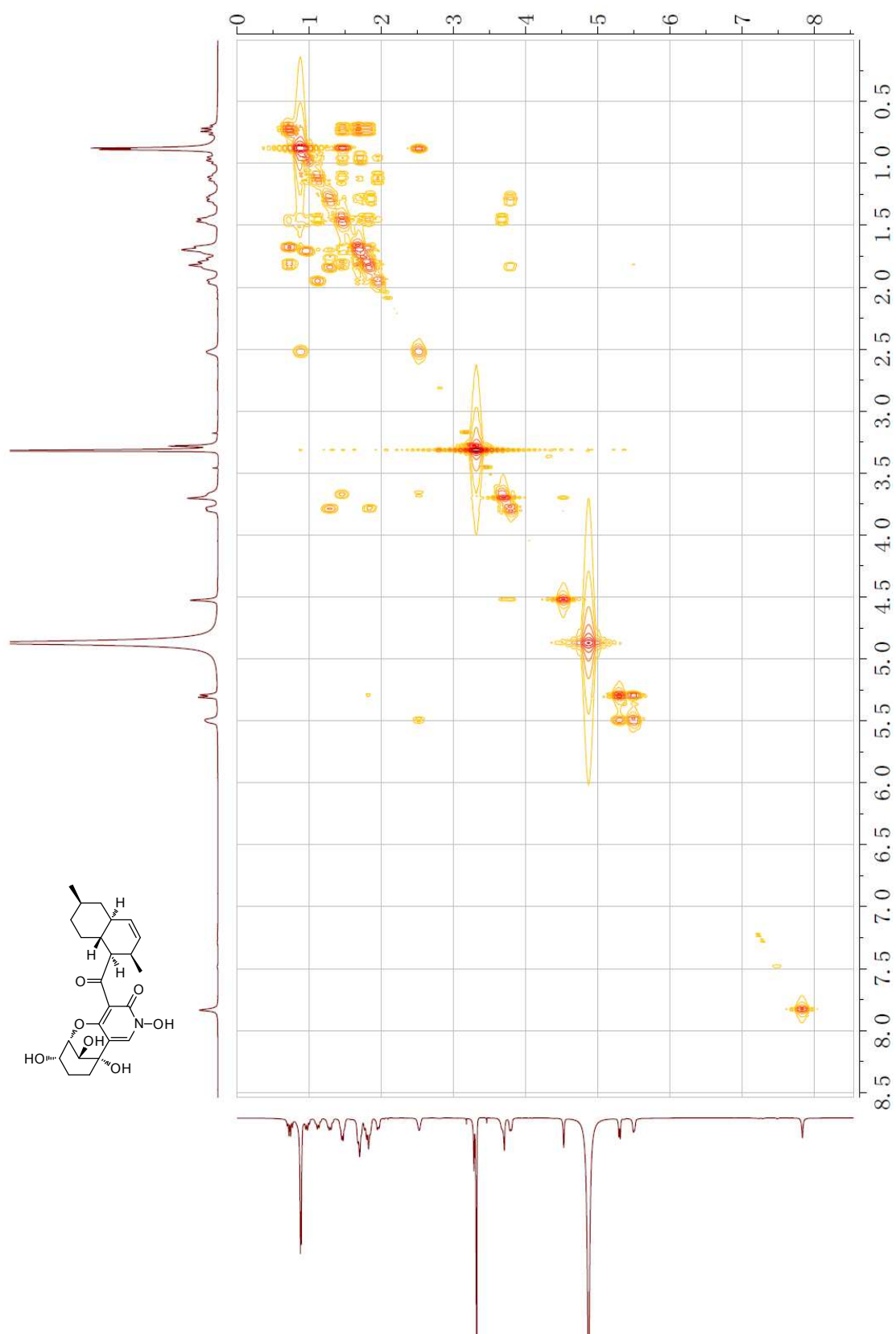


Figure S12. The HMBC spectrum of arthpyrone A (**1**) in CD₃OD

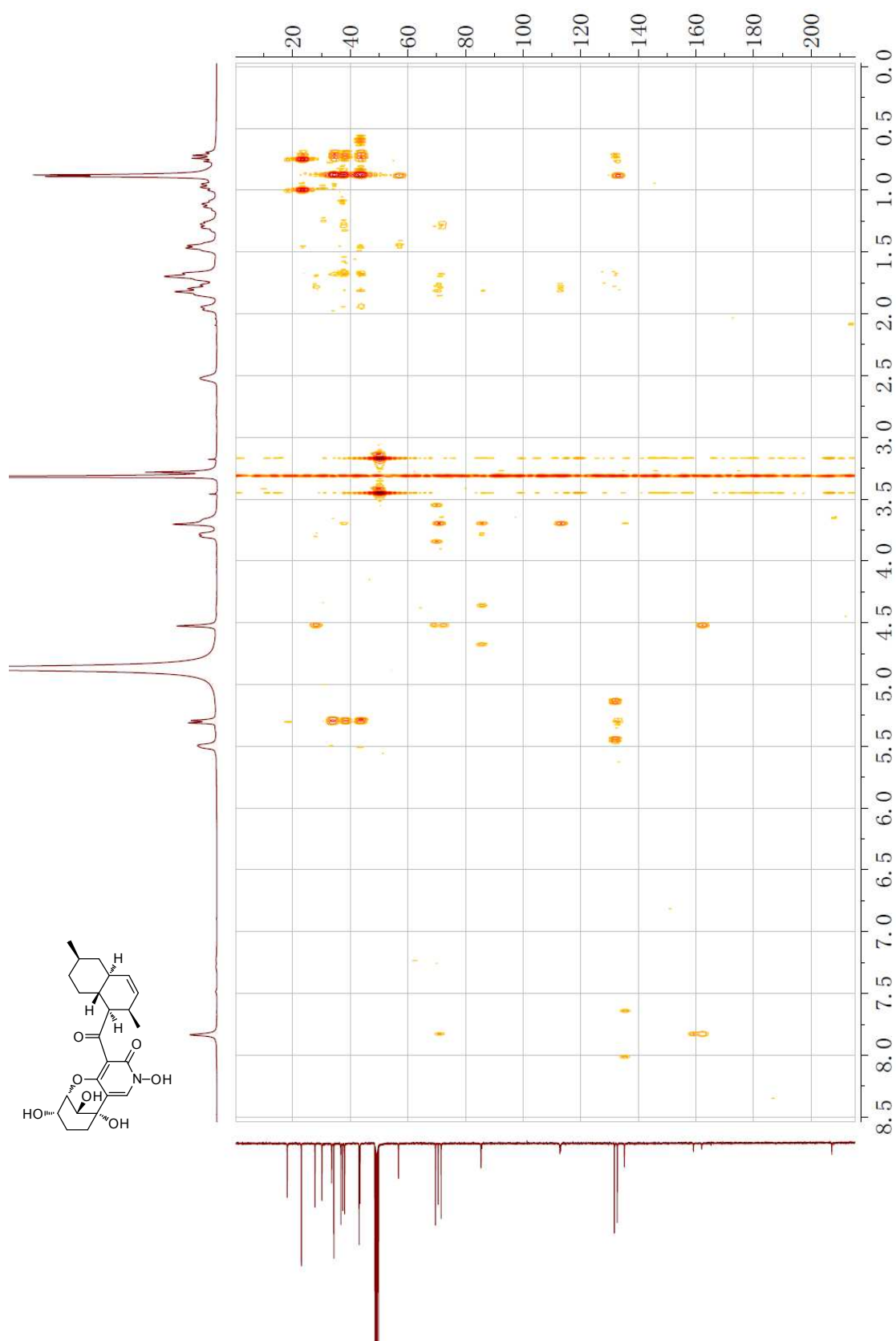


Figure S13. The NOESY spectrum of arthpyrone A (**1**) in CD₃OD

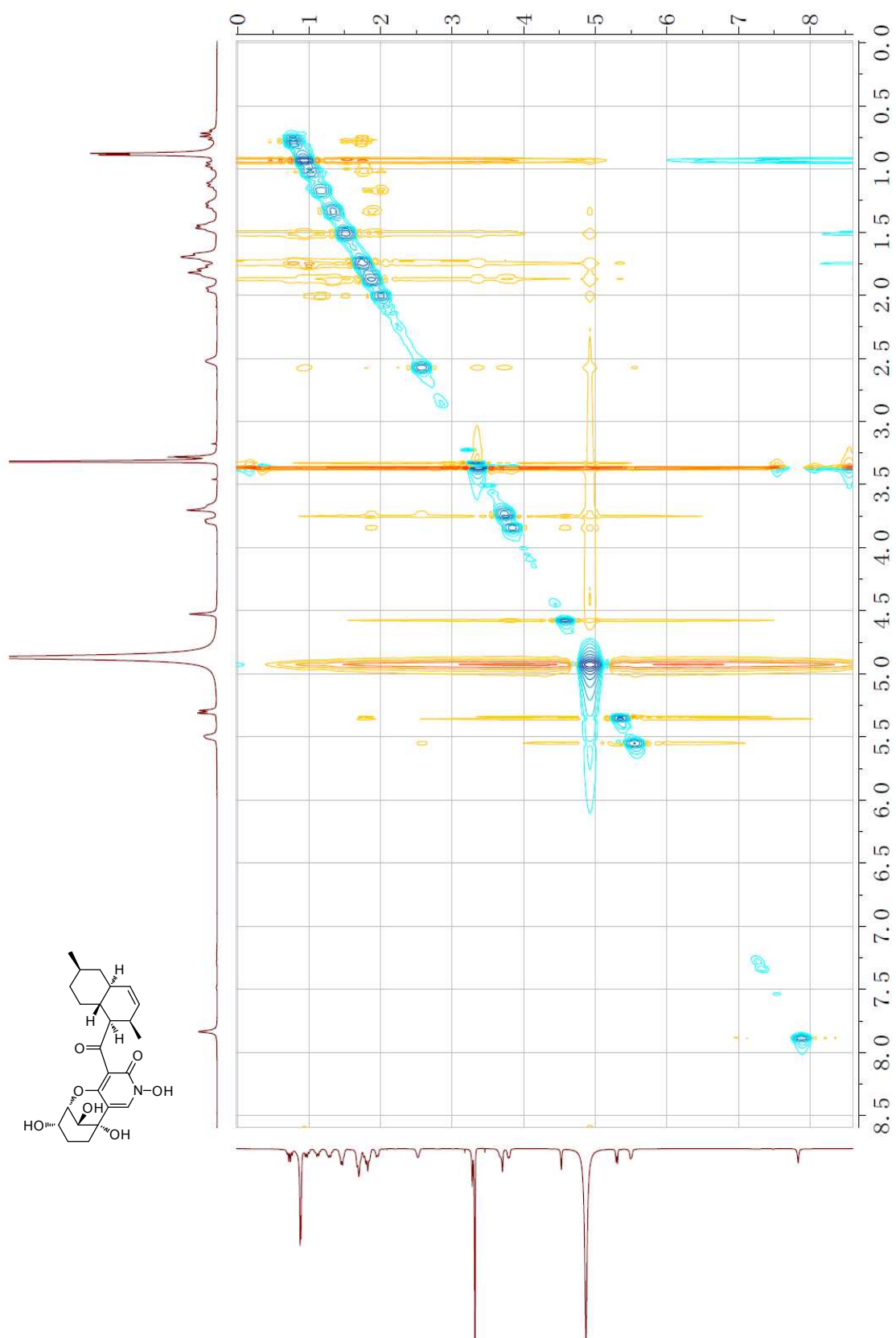
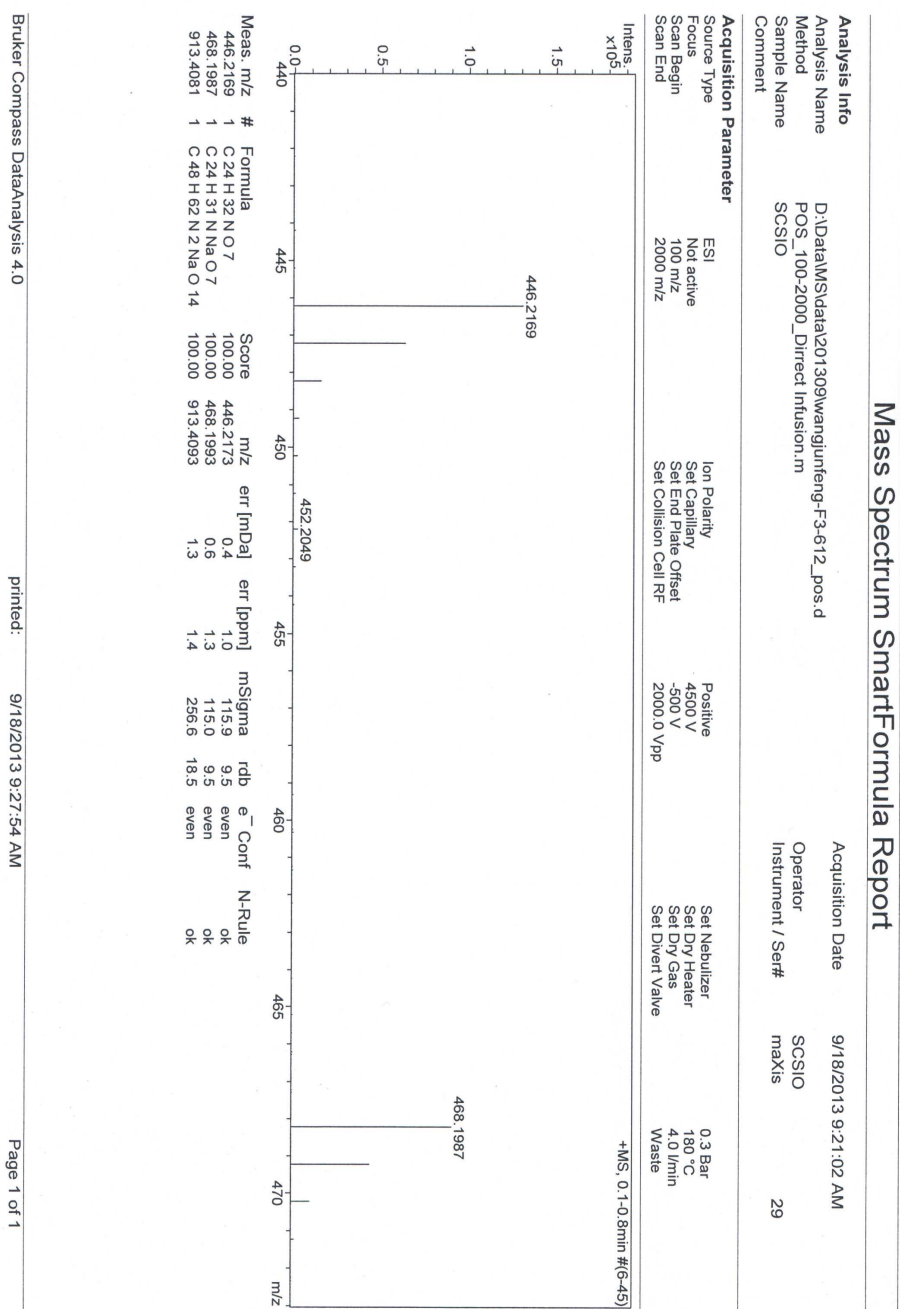


Figure S14. The HRESIMS spectrum of arthpyrone A (**1**)



Bruker Compass DataAnalysis 4.0

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Page 1 of 1

Figure S15. The ^1H NMR spectrum of arthpyrone B (**2**) in CD_3OD

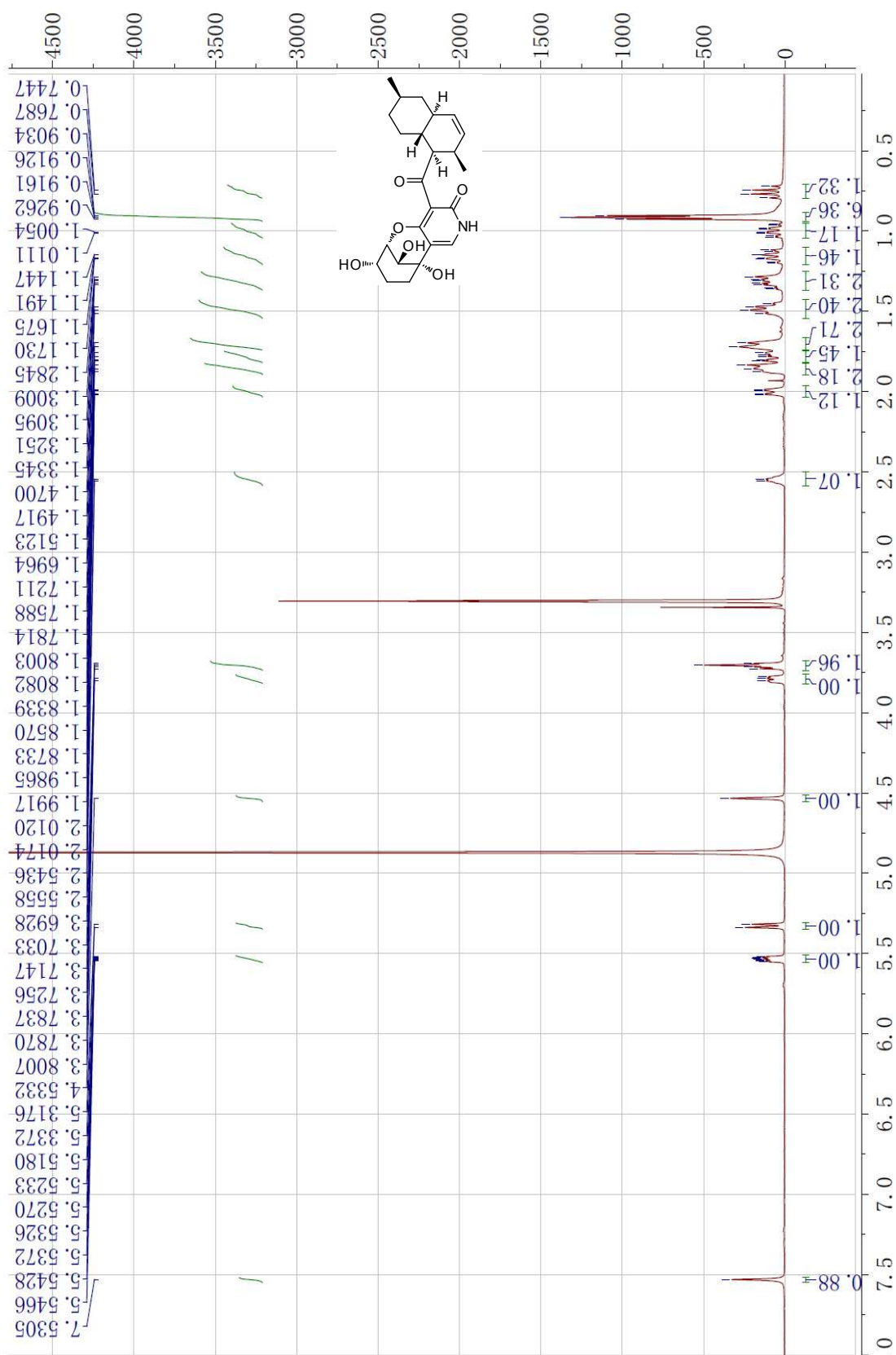


Figure S16. The ^{13}C NMR spectrum of arthpyrone B (**2**) in CD_3OD

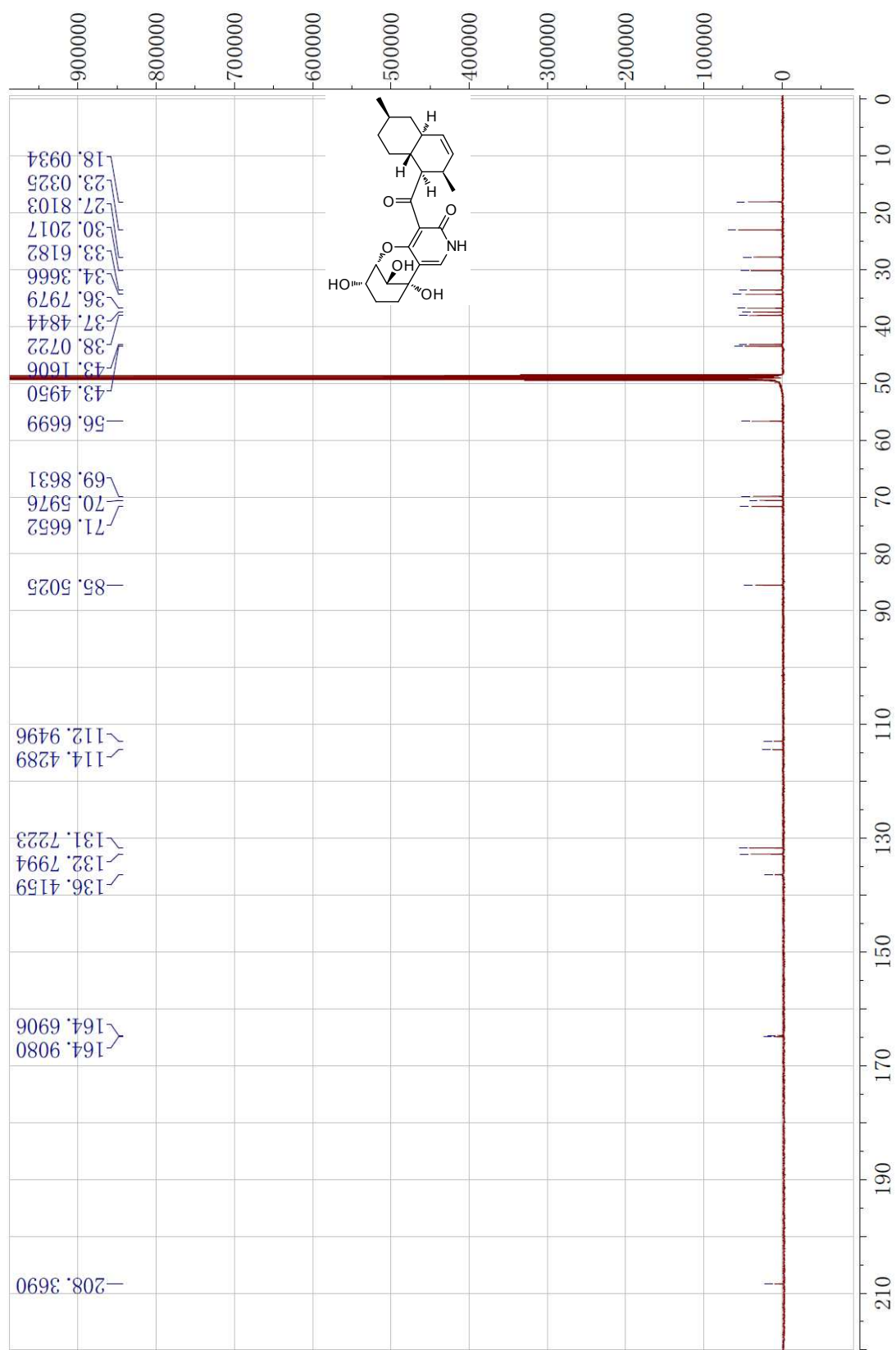


Figure S17. The HMQC spectrum of arthpyrone B (**2**) in CD₃OD

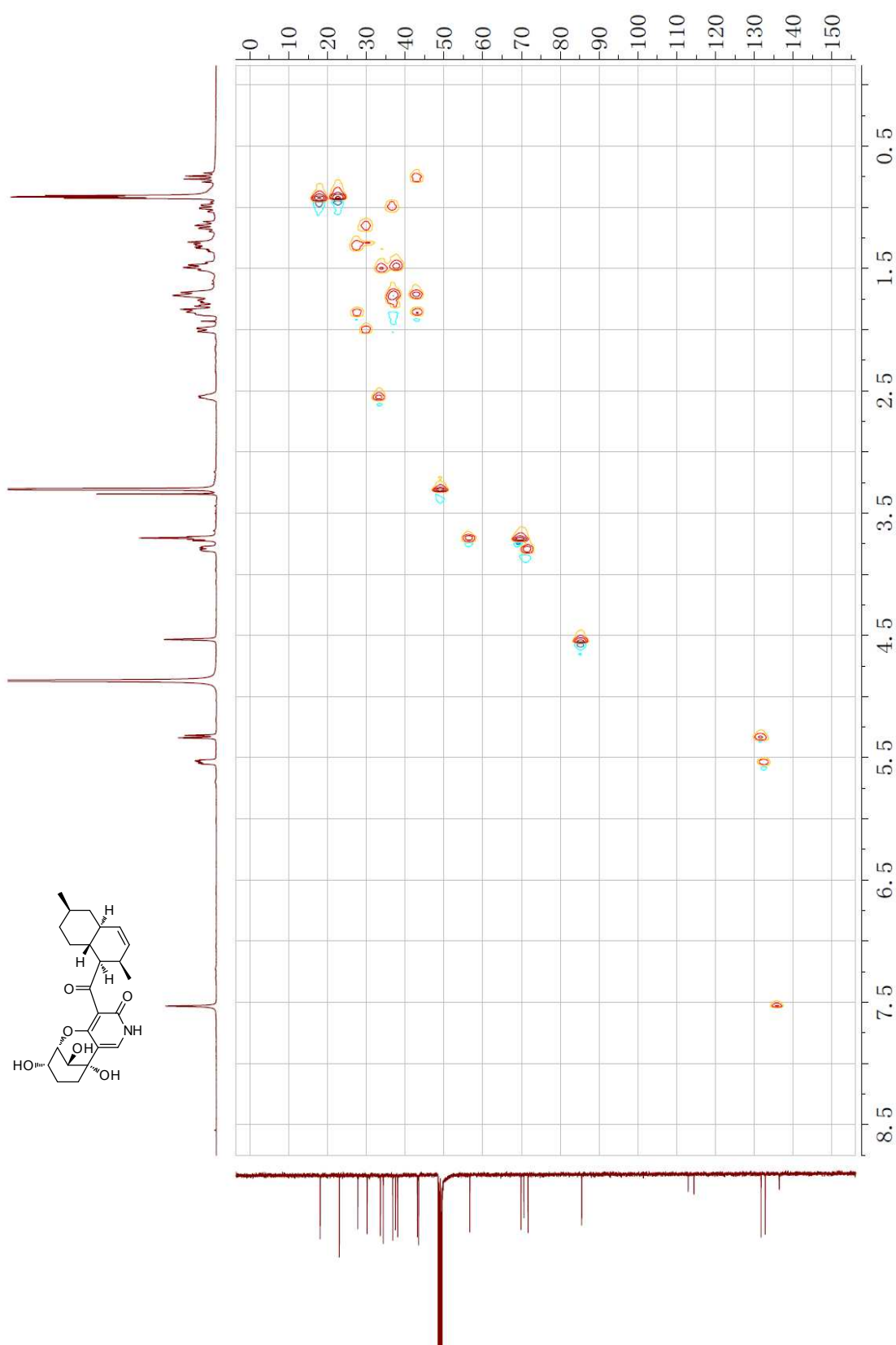


Figure S18. The ^1H - ^1H COSY spectrum of arthpyrone B (**2**) in CD_3OD

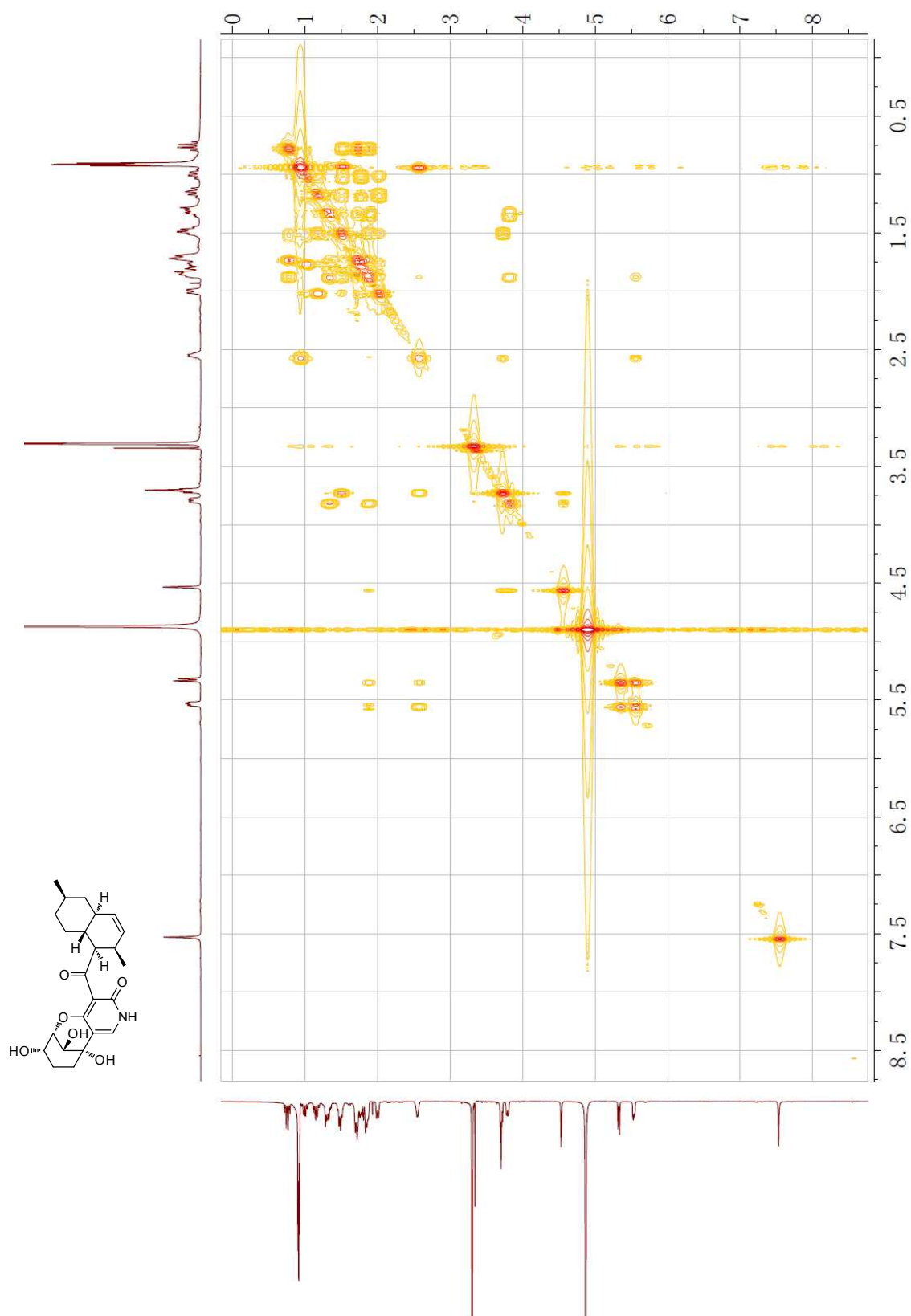


Figure S19. The HMBC spectrum of arthpyrone B (**2**) in CD₃OD

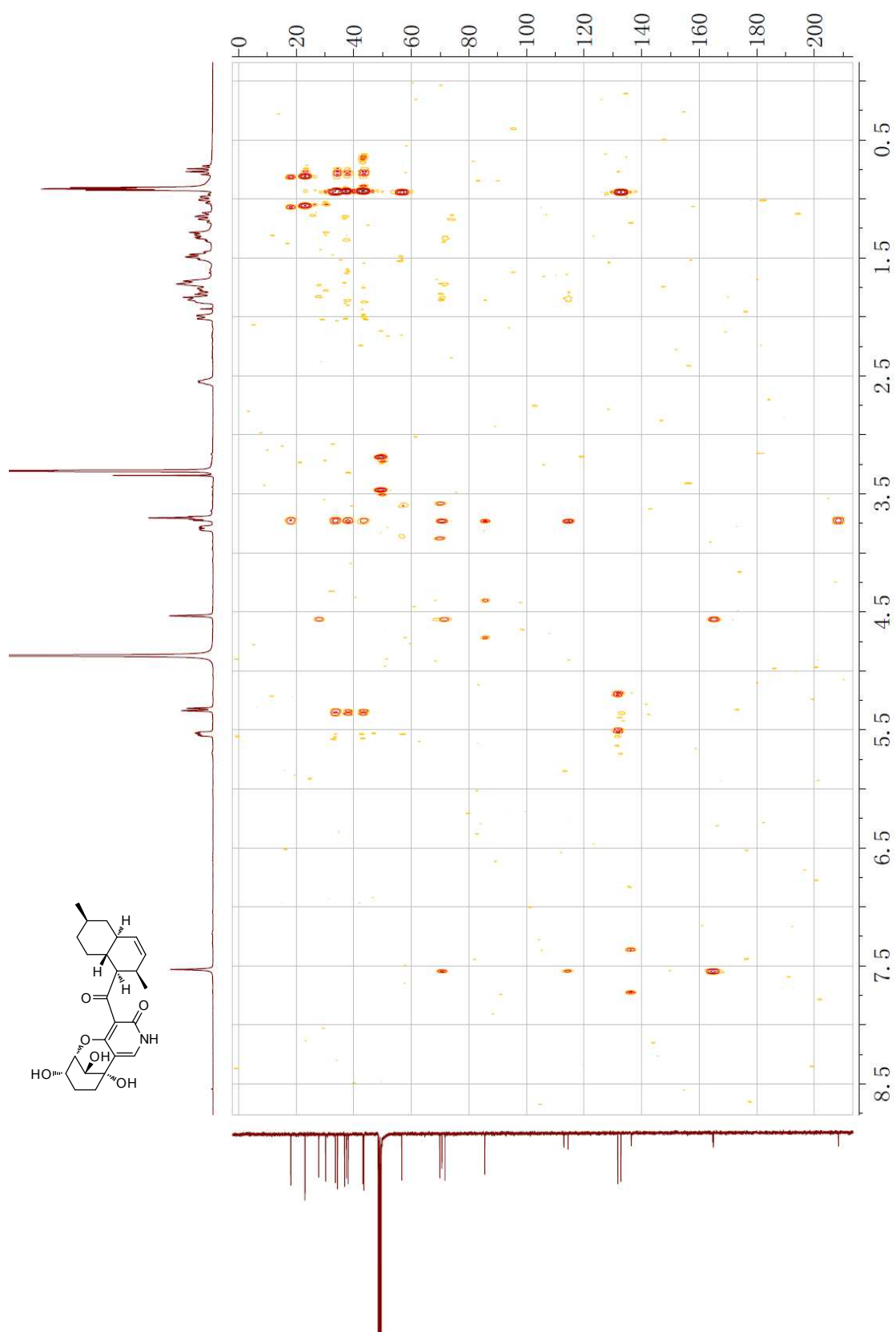


Figure S20. The NOESY spectrum of arthpyrone B (**2**) in CD₃OD

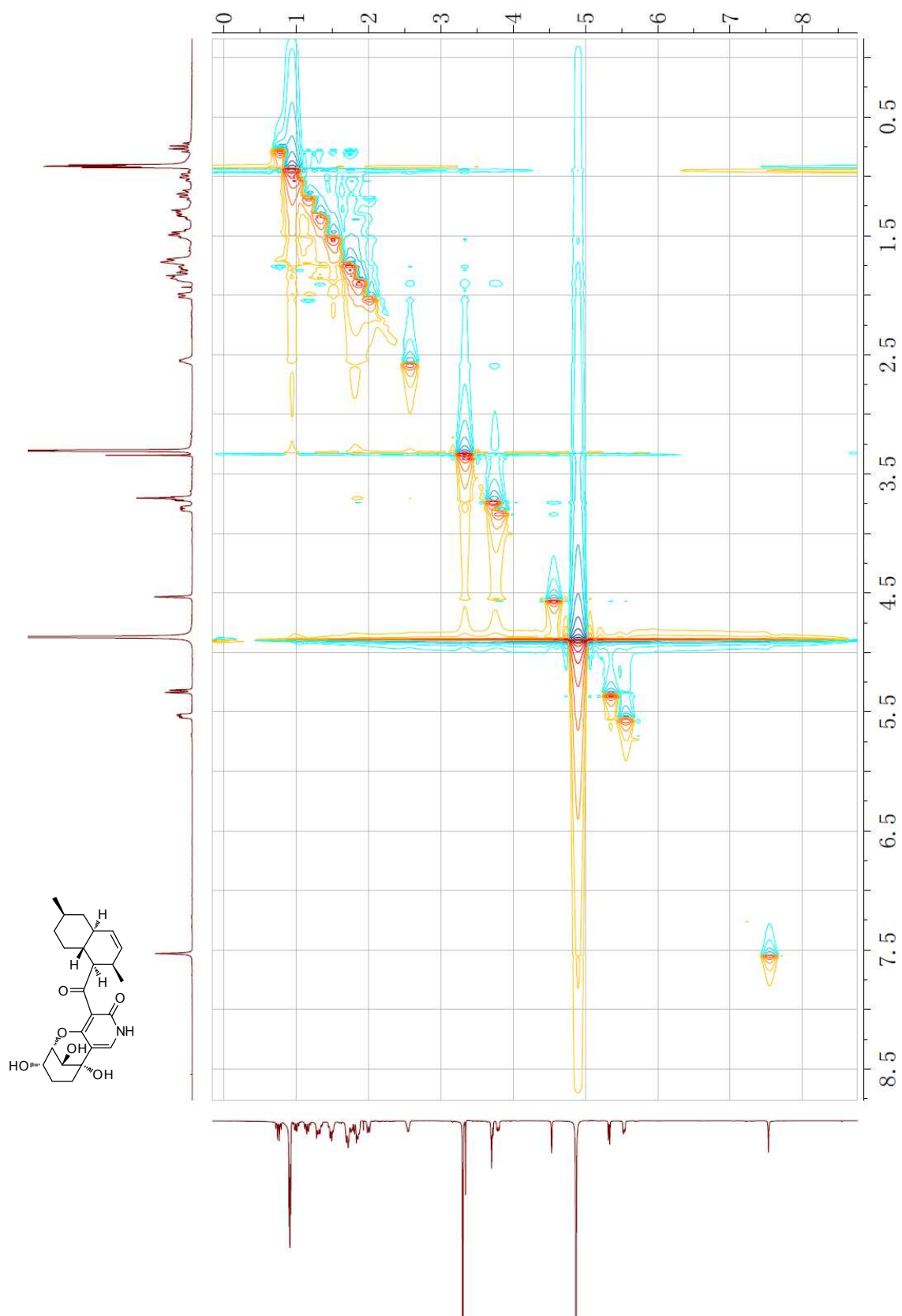


Figure S21. The HRESIMS spectrum of arthpyrone B (**2**)

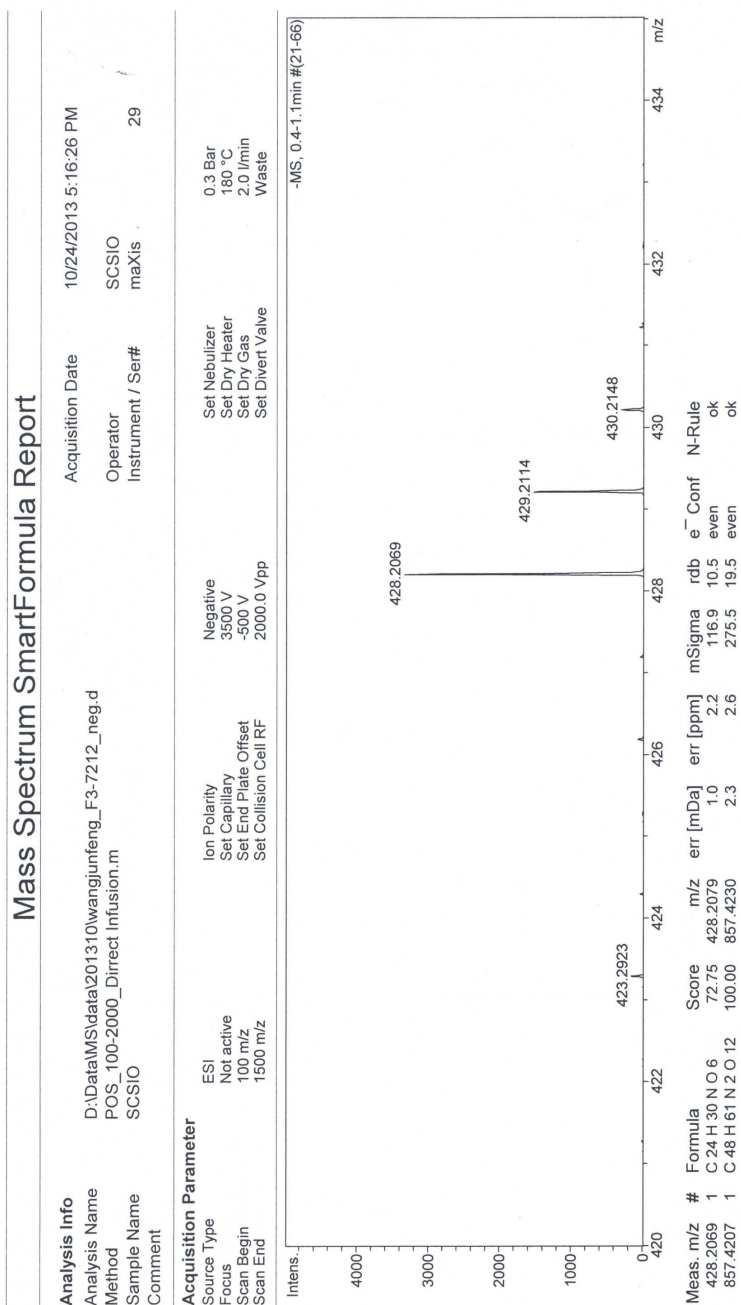


Figure S22. The ^1H NMR spectrum of arthpyrone C (**3**) in CD_3OD

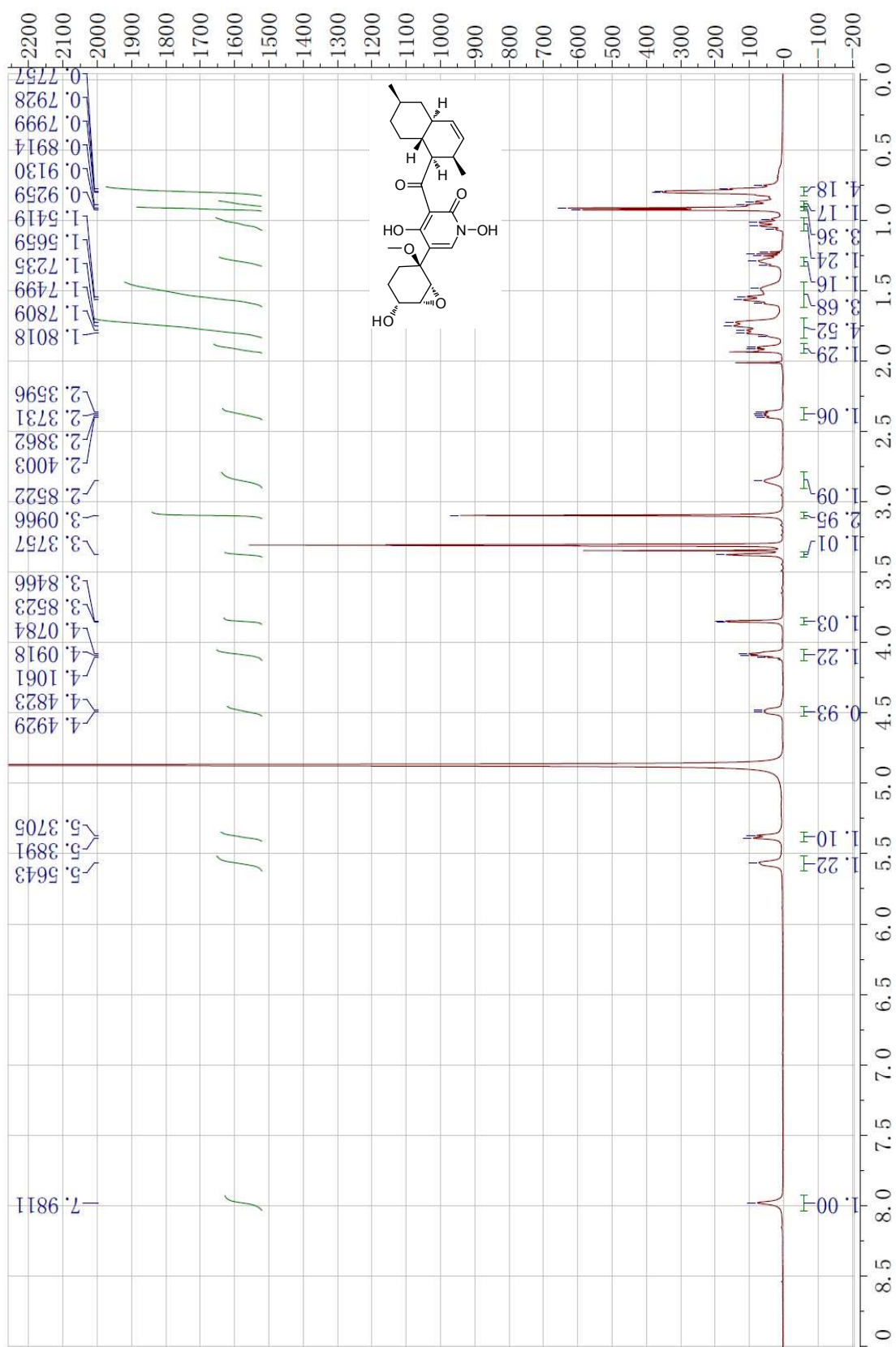


Figure S23. The ^{13}C NMR spectrum of arthpyrone C (**3**) in CD_3OD

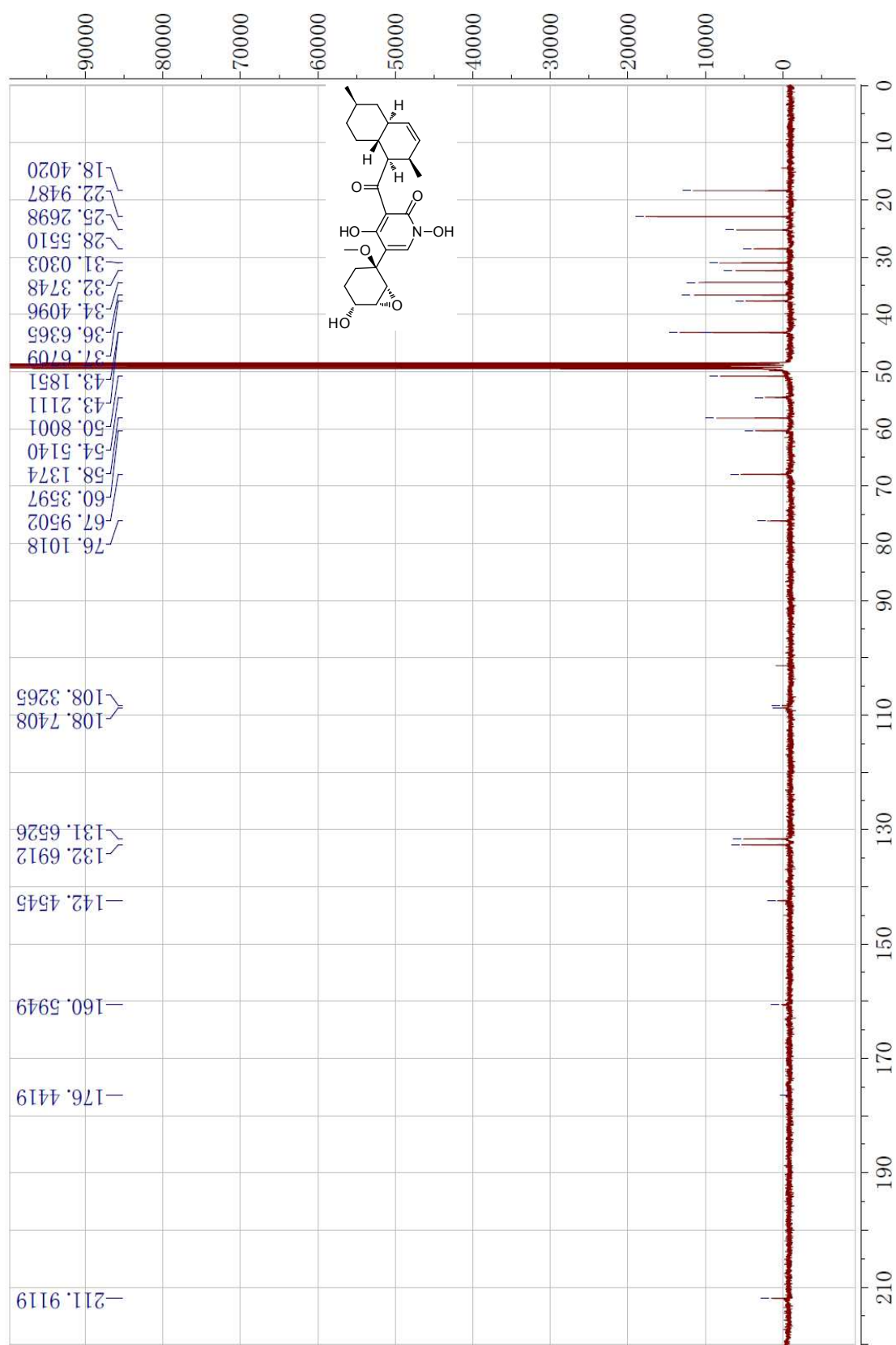


Figure S24. The HMQC spectrum of arthpyrone C (**3**) in CD₃OD

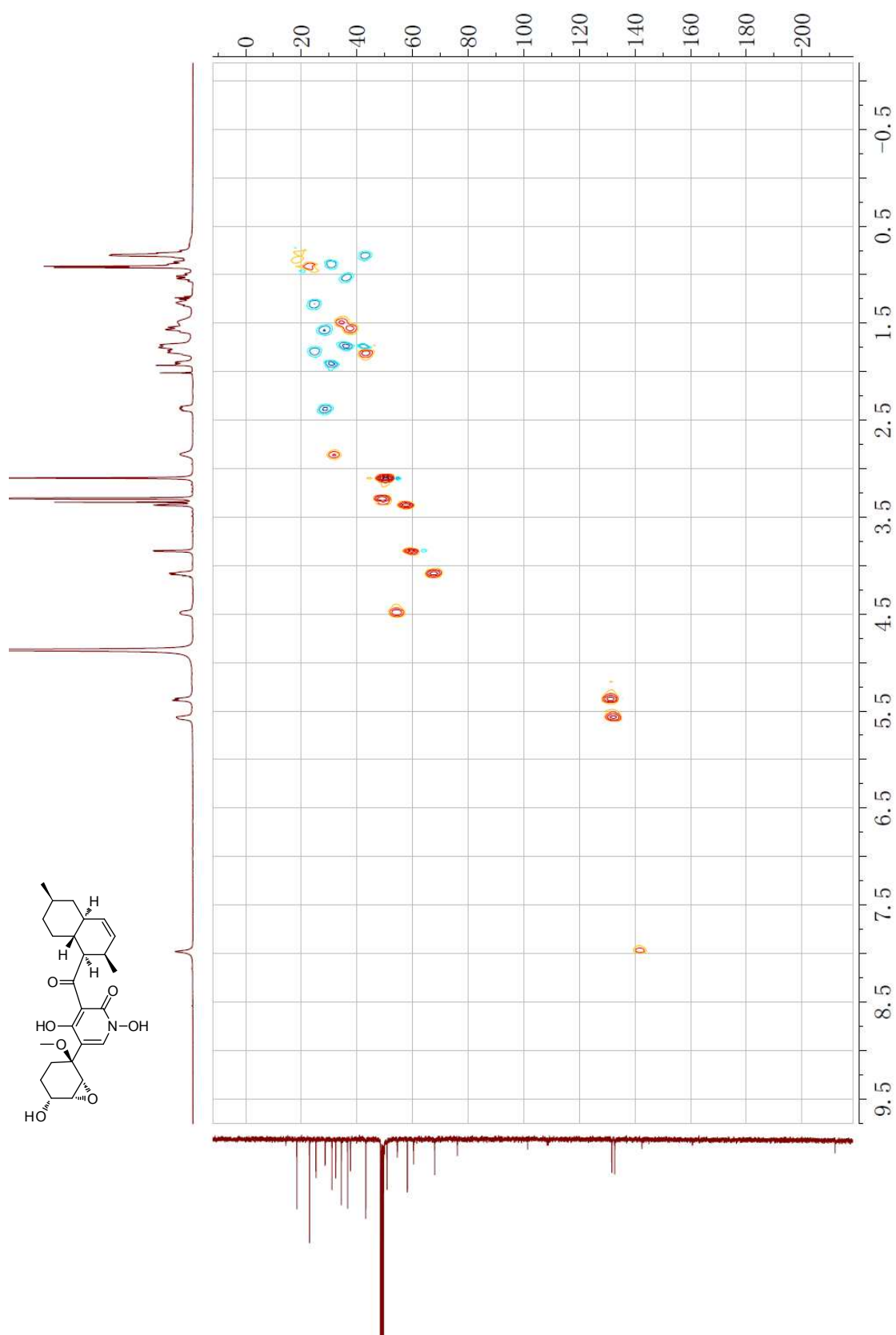


Figure S25. The ^1H - ^1H COSY spectrum of arthpyrone C (**3**) in CD_3OD

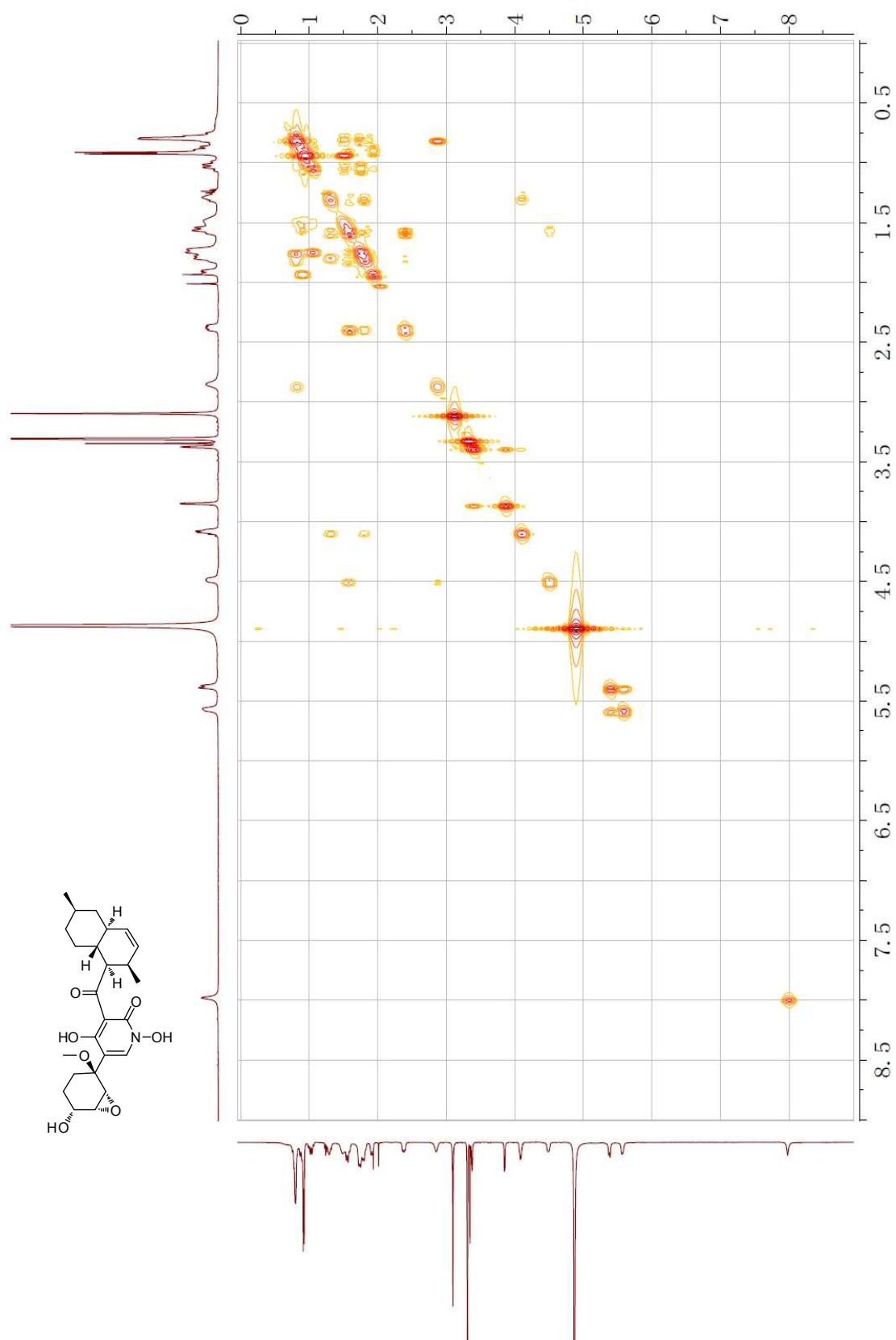


Figure S26. The HMBC spectrum of arthpyrone C (**3**) in CD₃OD

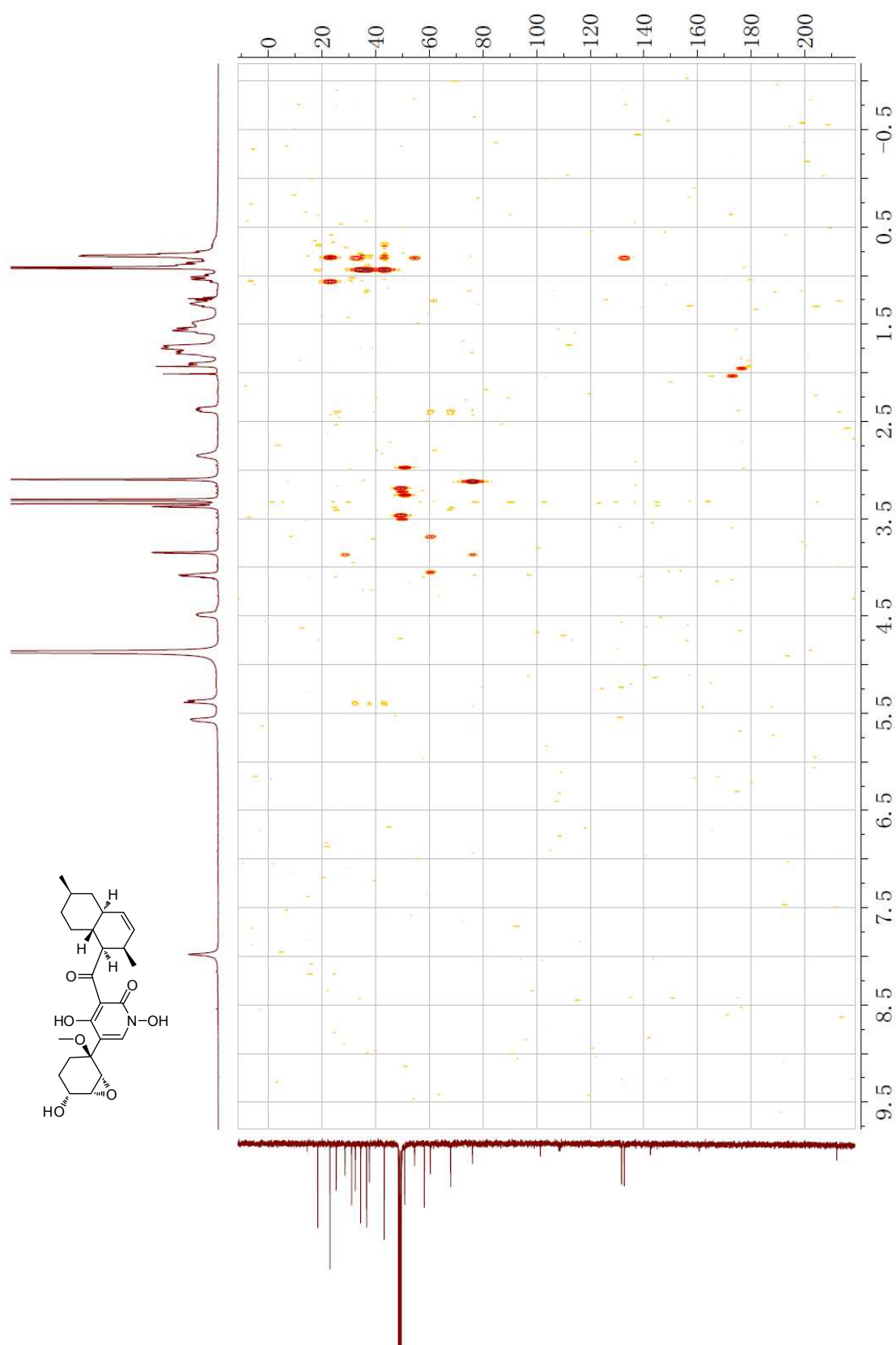


Figure S27. The NOESY spectrum of arthpyrone C (**3**) in CD₃OD

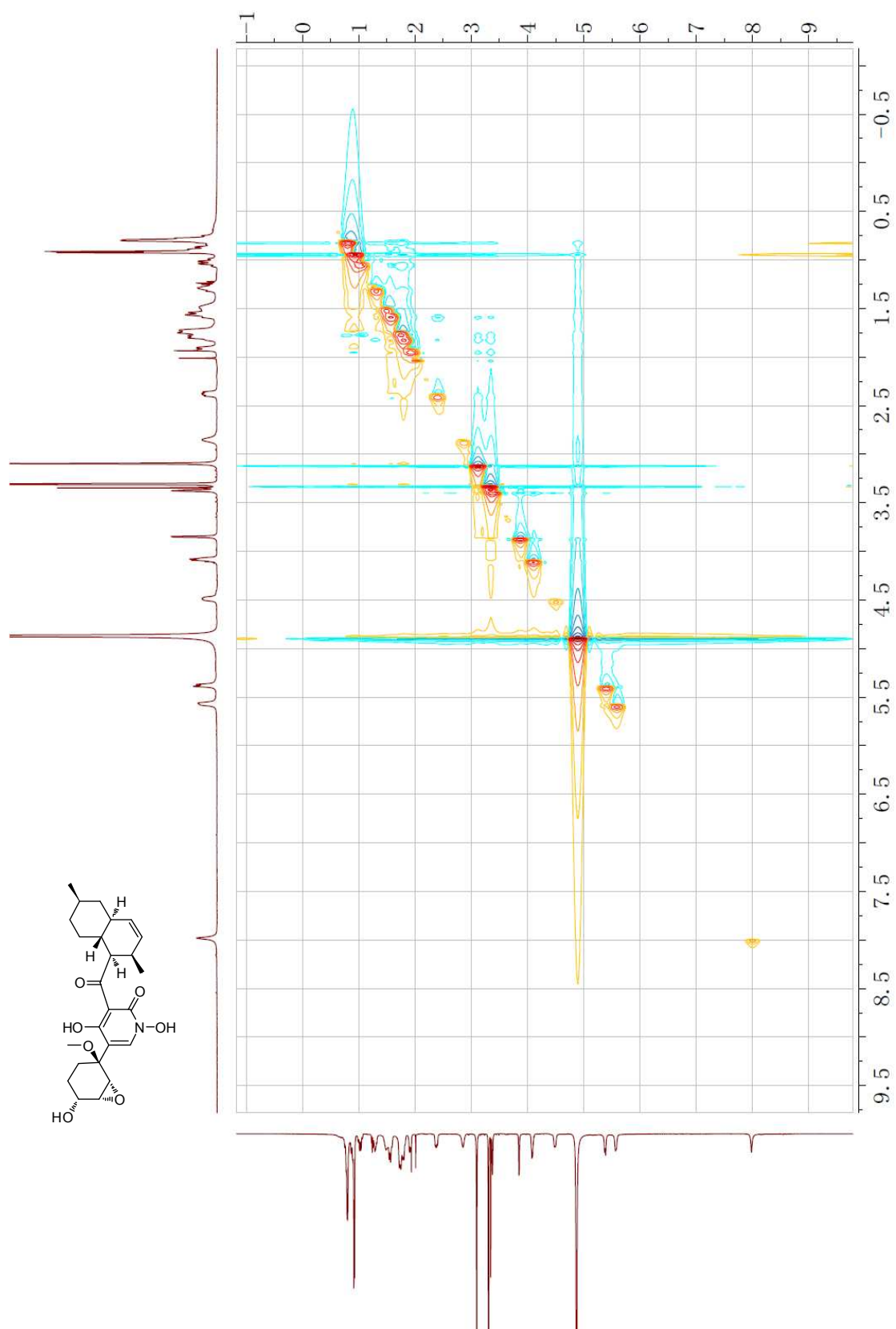


Figure S28. The HRESIMS spectrum of arthpyrone C (**3**)

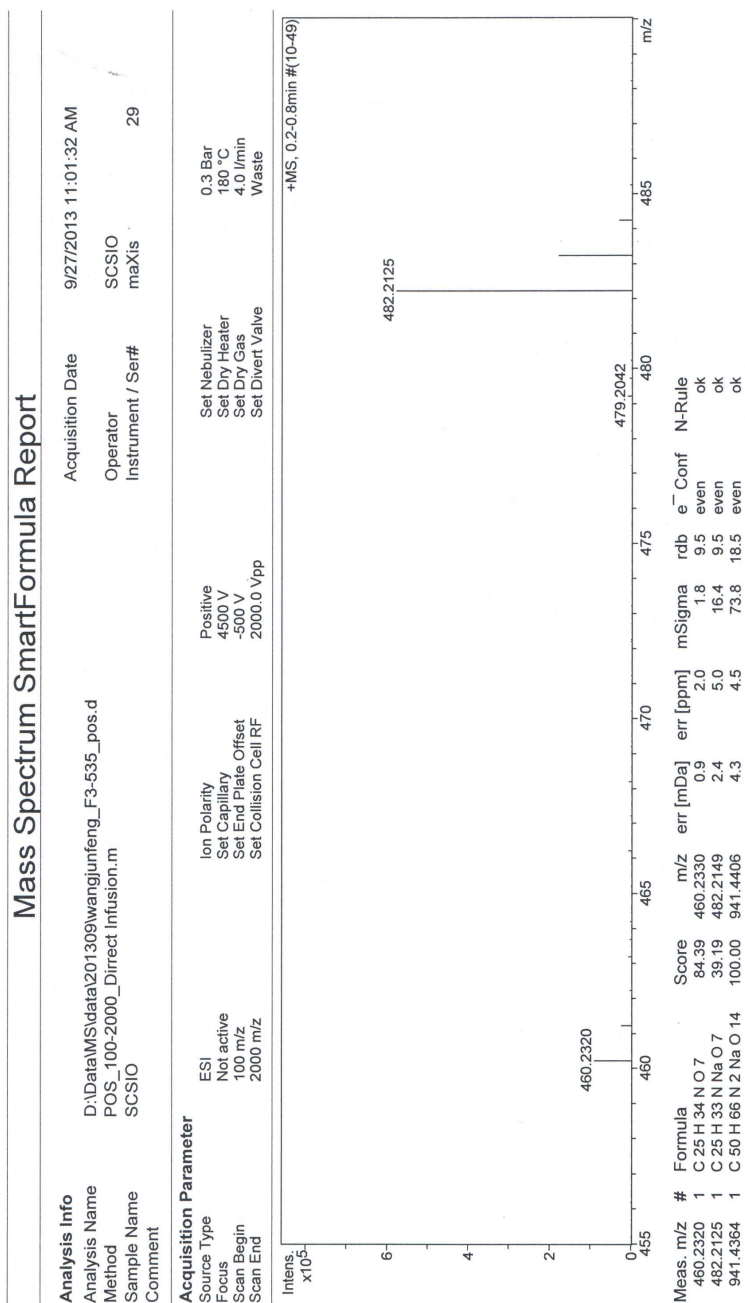


Figure S29. Analyzed compounds **1** and **2** by a chiralcel OD-H column

